



Sequence Listing US10069427.txt

SEQUENCE LISTING

<110> Famodu, Omolayo O.
Kinney, Anthony J.

<120> Genes Encoding Sterol Delta-14 Reductase in Plants

<130> 2119-4293

<140> 10/069,427

<141>

<150> 60/156,820

<151> 1999-09-30

<160> 10

<170> Microsoft Office 95

<210> 1

<211> 427

<212> DNA

<213> Glycine max

<220>

<221> unsure

<222> (360)

<223> n=a,c,g or t

<400> 1

```
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aactccgttc ctttgcttgt ggggttcttc acttacttgg ccgttgctgg atccattctc 120
cctggaaaac ttgttccttg cgttgcaacta ctcgatggaa ctcgcttaca ctattgctgc 180
aatggtctgc tctcgcttct tctgttgggt gcacttctcg ggatcggtgc caagatgggt 240
tttgtgtctc ccactgccat atcaaacaga ggacttgagc tgctgtccac aacttttgcc 300
ttcagttttc ttgtaaccct gatattgcat tttccgggt gcaagtcaca aagtaaagg 360
tcatactaa agcctcatct cagtgggaac ctgatacacg attggtgggt tgggaataca 420
actaaaa
```

<210> 2

<211> 126

<212> PRT

<213> Glycine max

<400> 2

```
Leu Gln Ala Leu Thr Pro Ser Trp Asn Ser Val Pro Leu Leu Val Gly
 1          5          10          15
```

```
Phe Phe Thr Tyr Leu Ala Val Ala Gly Ser Ile Leu Pro Gly Lys Leu
 20          25          30
```

```
Val Pro Gly Val Ala Leu Leu Asp Gly Thr Arg Leu His Tyr Cys Cys
 35          40          45
```

```
Asn Gly Leu Leu Ser Leu Leu Leu Val Ala Leu Leu Gly Ile Gly
 50          55          60
```

```
Ala Lys Met Gly Phe Val Ser Pro Thr Ala Ile Ser Asn Arg Gly Leu
 65          70          75          80
```

```
Glu Leu Leu Ser Thr Thr Phe Ala Phe Ser Phe Leu Val Thr Leu Ile
```

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85

90

95

Leu His Phe Ser Gly Cys Lys Ser Gln Ser Lys Gly Ser Ser Leu Lys
 100 105 110

Pro His Leu Ser Gly Asn Leu Ile His Asp Trp Trp Phe Gly
 115 120 125

<210> 3

<211> 667

<212> DNA

<213> Zea mays

<400> 3

ccacgcgtcc ggaagaacaa agtagagctg tcccttttgt ctggtctagc taacttatgc 60
 atctttctta ttggctacct agtggtccga ggagctaaca agcaaaaaca tgtgttcaag 120
 aaggaccca aagctcctat atggggaaaa cctcccaaag ttgtcggggg aaagctacta 180
 gcatctgggt actggggcat cgcaaggcac tgcaattatc tcggagacct gctgctagca 240
 ctttcgttca gcttgccctg tggagtgaat tccgtggtcc catacttcta cccacgtac 300
 ctgctcattc tactggctct gagggaaaag cgcgatgagg cgagggtgct gcagaagtac 360
 agggagatct gggcagagta ctgcaagctc gtgccgtgga ggatcctgcc ttatgtgtac 420
 tgaagagacg gtagaaacca aggcagctca tggccctggg ccagctgtaa acctattttt 480
 gtttgccctt aaccagttgg tgaatgttga tgtagcactc ggtaaactgt gaccgtgcaa 540
 acttttgtaa ttgttgggtc atacatgttt ggaatcgtga atcagaccgc ctacttgggt 600
 ggcaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 660
 aaaaaag 667

<210> 4

<211> 140

<212> PRT

<213> Zea mays

<400> 4

Pro Arg Val Arg Lys Asn Lys Val Glu Leu Ser Leu Leu Ser Gly Leu
 1 5 10 15

Ala Asn Leu Cys Ile Phe Leu Ile Gly Tyr Leu Val Phe Arg Gly Ala
 20 25 30

Asn Lys Gln Lys His Val Phe Lys Lys Asp Pro Lys Ala Pro Ile Trp
 35 40 45

Gly Lys Pro Pro Lys Val Val Gly Gly Lys Leu Leu Ala Ser Gly Tyr
 50 55 60

Trp Gly Ile Ala Arg His Cys Asn Tyr Leu Gly Asp Leu Leu Leu Ala
 65 70 75 80

Leu Ser Phe Ser Leu Pro Cys Gly Val Ser Ser Val Val Pro Tyr Phe
 85 90 95

Tyr Pro Thr Tyr Leu Leu Ile Leu Leu Val Leu Arg Glu Arg Arg Asp
 100 105 110

Glu Ala Arg Cys Ser Gln Lys Tyr Arg Glu Ile Trp Ala Glu Tyr Cys
 115 120 125

Lys Leu Val Pro Trp Arg Ile Leu Pro Tyr Val Tyr
 130 135 140

<210> 5

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<211> 1631
<212> DNA
<213> Glycine max

<400> 5
ccgcgttgga atttgcccat ctaaaacctc aatcttttac tgaaaagtct caactttgaa 60
ctcactcgaa gtgatgatgg agtcacacgt ggatctagggt tttctccttc aagctctcac 120
tccatcttgg aactccgttc ctttgcttgt ggggttcttc acttacttgg ccgttgctgg 180
atccattctc cctggaaaac ttgttcctgg cgttgcacta ctcgatggaa ctcgtctaca 240
ctattgctgc aatgggtctgc tctcgcttct tctgttggtt gcacttctcg ggatcgggtgc 300
caagatgggt tttgtgtctc ccactgccat atcagacaga ggacttgagc tgctgtccac 360
aacttttgcc ttcagttttc ttgtaaccct gatattgcat tttccgggtt gcaagtcaca 420
aagtaaagggt tcatcactaa agcctcatct cagtggaaac ctgatacacg attgggtgggt 480
tggatataca ctaaatccac agttcatggg tatcgacctc aaatttttct ttgtagagc 540
tggaatgatg ggaatggctac ttatcaattt atctattctt atgaagagca ttcaagatgg 600
tactttgagc cagtcaatga ttctctacca gctattctgt gcactataca tcctggacta 660
ttttgtacat gaagagtaca tgacatccac ctgggacata attgcagaga gactgggctt 720
catgttggtc tttggagatt tagtgtggat tcttttctct ttcagcatac agggatgggtg 780
gctcttgatg aacagtgtgg agttaacacc agctgccatt gtagctaatt gctttgtgtt 840
cctgattgga tacatgggat ttcgaggagc aaacaagcaa aagcatgtgt tcaaaaagaa 900
tccaaaggct cctatctggg gtaagcctcc aaaagtcatt ggtggaaagc tacttgcttc 960
tggtaattgg ggtattgcta gacactgtaa ttacctaggg gatttgatgc ttgctctctc 1020
ctttagctta ccatgtggga taagtccacc aattccatac ttctatccaa tttatcttct 1080
tattctgtta atctggagag agagaaggga tgaagctcgt tgcgccgaga agtatagaga 1140
gatatgggcc gagtatcgta aacttggtcc atggagaata ttgccttacg tttattagga 1200
tgaaaaaaa aagggtcttc ccatgaattc ttcattctgc cgatgttatt aagcacttcg 1260
atgtaaattg gttcttggtc ttgtggtttc aatcttggat cttttcttat tgagccatgt 1320
agctgcagga gagtgtttcg agggatttat cttaccatct atatttgtgt atcattatgc 1380
tgcagcctgc aggccttcat tttcaatgg ccaactcttt ttgacttggt ctatttgttt 1440
ttagatgaga atttcatggt caaagctcct aggccttaaaa aaacagtgtc atgttctatg 1500
ggaagtgcag gaagcaattc ggggactgca ggaagcaatt gcctttacat tgatatgctc 1560
aatggtactt taggcccttt aatgttcttg cttttcattt gtgagttatt attggcccca 1620
tttcatttgc a 1631

<210> 6
<211> 374
<212> PRT
<213> Glycine max

<400> 6
Met Met Glu Ser His Val Asp Leu Gly Phe Leu Leu Gln Ala Leu Thr
1 5 10 15
Pro Ser Trp Asn Ser Val Pro Leu Leu Val Gly Phe Phe Thr Tyr Leu
20 25 30
Ala Val Ala Gly Ser Ile Leu Pro Gly Lys Leu Val Pro Gly Val Ala
35 40 45
Leu Leu Asp Gly Thr Arg Leu His Tyr Cys Cys Asn Gly Leu Leu Ser
50 55 60
Leu Leu Leu Leu Val Ala Leu Leu Gly Ile Gly Ala Lys Met Gly Phe
65 70 75 80
Val Ser Pro Thr Ala Ile Ser Asp Arg Gly Leu Glu Leu Leu Ser Thr
85 90 95
Thr Phe Ala Phe Ser Phe Leu Val Thr Leu Ile Leu His Phe Ser Gly
100 105 110
Cys Lys Ser Gln Ser Lys Gly Ser Ser Leu Lys Pro His Leu Ser Gly

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115      120      125
Asn Leu Ile His Asp Trp Trp Phe Gly Ile Gln Leu Asn Pro Gln Phe
130      135      140
Met Gly Ile Asp Leu Lys Phe Phe Phe Val Arg Ala Gly Met Met Gly
145      150      155      160
Trp Leu Leu Ile Asn Leu Ser Ile Leu Met Lys Ser Ile Gln Asp Gly
165      170      175
Thr Leu Ser Gln Ser Met Ile Leu Tyr Gln Leu Phe Cys Ala Leu Tyr
180      185      190
Ile Leu Asp Tyr Phe Val His Glu Glu Tyr Met Thr Ser Thr Trp Asp
195      200      205
Ile Ile Ala Glu Arg Leu Gly Phe Met Leu Val Phe Gly Asp Leu Val
210      215      220
Trp Ile Pro Phe Ser Phe Ser Ile Gln Gly Trp Trp Leu Leu Met Asn
225      230      235      240
Ser Val Glu Leu Thr Pro Ala Ala Ile Val Ala Asn Cys Phe Val Phe
245      250      255
Leu Ile Gly Tyr Met Val Phe Arg Gly Ala Asn Lys Gln Lys His Val
260      265      270
Phe Lys Lys Asn Pro Lys Ala Pro Ile Trp Gly Lys Pro Pro Lys Val
275      280      285
Ile Gly Gly Lys Leu Leu Ala Ser Gly Tyr Trp Gly Ile Ala Arg His
290      295      300
Cys Asn Tyr Leu Gly Asp Leu Met Leu Ala Leu Ser Phe Ser Leu Pro
305      310      315      320
Cys Gly Ile Ser Ser Pro Ile Pro Tyr Phe Tyr Pro Ile Tyr Leu Leu
325      330      335
Ile Leu Leu Ile Trp Arg Glu Arg Arg Asp Glu Ala Arg Cys Ala Glu
340      345      350
Lys Tyr Arg Glu Ile Trp Ala Glu Tyr Arg Lys Leu Val Pro Trp Arg
355      360      365
Ile Leu Pro Tyr Val Tyr
370

```

<210> 7
 <211> 1364
 <212> DNA
 <213> Glycine max

<400> 7
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 aactccgttc ctttgcttgt ggggttcttc acttacttgg ccgttgctgg atccattctc 180
 cctggaacac ttgttcttgg cgttgcacta ctcgatggaa ctcgtctaca ctattgctgc 240

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```

aatggtctgc tctcgcttct tctgttggtt gcacttctcg ggatcgggtg caagatgggt 300
tttgtgtctc ccactgccat atcagacaga ggacttgagc tgctgtccac aacttttgcc 360
ttcagttttc ttgtaaccct gatattgcat ttttccggtt gcaagtcaca aagtaaaggc 420
tcatcactaa agcctcatct cagtggaaac ctgatacacg attggtgggt tgggtatacaa 480
ctaaatccac agttcatggg tatcgacctc aaagctggaa tgatgggatg gctacttatc 540
aatttatcta ttcttatgaa gagcattcaa gatggtactt tgagccagtc aatgattctc 600
taccagctat tctgtgcact atacatcctg gactattttg tacatgaaga gtacatgaca 660
tccacctggg acataattgc agagagactg ggcttcatgt tggcttttgg agatttagtg 720
tggattcctt tctctttcag catacagggg tgggtggctct tgatgaacag tgtggagtta 780
acaccagctg ccattgtagc taattgcttt gtgttcctga ttggatacat ggtatttcga 840
ggagcaaaca agcaaaaagca tgtgttcaaa aagaatccaa aggctcctat ctggggtaag 900
cctccaaaag tcattggtgg aaagctactt gcttctgggt attgggggat tgctagacac 960
tgtaattacc taggggattt gatgcttgct ctctccttta gcttaccatg tgggataagt 1020
tcaccaattc catacttcta tccaatttat ctcttatttc tgtaaatctg gagagagaga 1080
acggatgaag ctcgttgccg cgagaagtat agagagatat gggccgagta tcgtaaactt 1140
gttccatgga gaattattgc ttacgtttat taggatgaaa aaaaaaaggg cttcaccatg 1200
aattcttcat cttgccgatg ttattaagca cttcgatgta aattggttct tgttcttggt 1260
gtttcaatct tggatctttt cttattgagc catgtagctg caggagagtg tttcgaggga 1320
tttatcttac catctatatt tgtgtaaaaa aaaaaaaaaa aaaa 1364

```

<210> 8
 <211> 369
 <212> PRT
 <213> Glycine max

<400> 8
 Met Met Glu Ser His Val Asp Leu Gly Phe Leu Leu Gln Ala Leu Thr
 1 5 10 15
 Pro Ser Trp Asn Ser Val Pro Leu Leu Val Gly Phe Phe Thr Tyr Leu
 20 25 30
 Ala Val Ala Gly Ser Ile Leu Pro Gly Lys Leu Val Pro Gly Val Ala
 35 40 45
 Leu Leu Asp Gly Thr Arg Leu His Tyr Cys Cys Asn Gly Leu Leu Ser
 50 55 60
 Leu Leu Leu Leu Val Ala Leu Leu Gly Ile Gly Ala Lys Met Gly Phe
 65 70 75 80
 Val Ser Pro Thr Ala Ile Ser Asp Arg Gly Leu Glu Leu Leu Ser Thr
 85 90 95
 Thr Phe Ala Phe Ser Phe Leu Val Thr Leu Ile Leu His Phe Ser Gly
 100 105 110
 Cys Lys Ser Gln Ser Lys Gly Ser Ser Leu Lys Pro His Leu Ser Gly
 115 120 125
 Asn Leu Ile His Asp Trp Trp Phe Gly Ile Gln Leu Asn Pro Gln Phe
 130 135 140
 Met Gly Ile Asp Leu Lys Ala Gly Met Met Gly Trp Leu Leu Ile Asn
 145 150 155 160
 Leu Ser Ile Leu Met Lys Ser Ile Gln Asp Gly Thr Leu Ser Gln Ser
 165 170 175
 Met Ile Leu Tyr Gln Leu Phe Cys Ala Leu Tyr Ile Leu Asp Tyr Phe
 180 185 190

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Val His Glu Glu Tyr Met Thr Ser Thr Trp Asp Ile Ile Ala Glu Arg
195 200 205
Leu Gly Phe Met Leu Val Phe Gly Asp Leu Val Trp Ile Pro Phe Ser
210 215 220
Phe Ser Ile Gln Gly Trp Trp Leu Leu Met Asn Ser Val Glu Leu Thr
225 230 235 240
Pro Ala Ala Ile Val Ala Asn Cys Phe Val Phe Leu Ile Gly Tyr Met
245 250 255
Val Phe Arg Gly Ala Asn Lys Gln Lys His Val Phe Lys Lys Asn Pro
260 265 270
Lys Ala Pro Ile Trp Gly Lys Pro Pro Lys Val Ile Gly Gly Lys Leu
275 280 285
Leu Ala Ser Gly Tyr Trp Gly Ile Ala Arg His Cys Asn Tyr Leu Gly
290 295 300
Asp Leu Met Leu Ala Leu Ser Phe Ser Leu Pro Cys Gly Ile Ser Ser
305 310 315 320
Pro Ile Pro Tyr Phe Tyr Pro Ile Tyr Leu Leu Ile Leu Leu Ile Trp
325 330 335
Arg Glu Arg Thr Asp Glu Ala Arg Cys Ala Glu Lys Tyr Arg Glu Ile
340 345 350
Trp Ala Glu Tyr Arg Lys Leu Val Pro Trp Arg Ile Leu Pro Tyr Val
355 360 365

Tyr
369

<210> 9
<211> 430
<212> PRT
<213> Ascobolus immersus

<400> 9
Met Gly Gly Lys Asp Tyr Glu Phe Gly Gly Pro Ile Gly Thr Gly Val
1 5 10 15
Leu Met Leu Ile Leu Pro Pro Ile Ser His Tyr Leu His Phe Leu Ile
20 25 30
Thr Pro Arg Gly Ala Pro Pro Pro Glu Phe Trp Ser Ala Pro Leu Glu
35 40 45
Thr Leu Lys Ser Val Thr Pro Thr Phe Ser Ser Leu Phe Ser Leu His
50 55 60
Ala Thr Leu Ala Val Ala Ala Tyr Tyr Leu Leu Val Ala Leu Met
65 70 75 80
Tyr Val Leu Pro Ala Glu Ile Ala Glu Gly Val Val Leu Lys Asp Gly
85 90 95
Ser Arg Leu Lys Tyr Arg Cys Asn Ala Phe Thr Thr Phe Leu Val Phe
100 105 110

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Phe Thr Phe Leu Gly Thr Met Thr Val Leu Glu Gly Pro Thr Trp Trp
115 120 125

Phe Trp Ser Tyr Leu Thr Asp Asn Phe Ala Gln Leu Gln Ser Ala Ser
130 135 140

Ile Val Phe Ser Tyr Ala Met Ser Leu Trp Val Tyr Ile Arg Ser Tyr
145 150 155 160

Arg Pro Met Pro Lys Gly Lys Glu Val Ile Leu Ser Pro Val Gly Phe
165 170 175

Lys Gly Asn His Ile His Asp Phe Trp Met Gly Arg Glu Leu Asn Pro
180 185 190

Arg Ile Gly Glu Trp Leu Asp Ile Lys Gln Leu His Glu Leu Arg Pro
195 200 205

Gly Leu Met Gly Trp Ile Leu Phe Asn Leu Ala Trp Thr Val Lys Gln
210 215 220

Tyr Asn Thr His Gly Phe Val Ser Asp Ser Ile Val Leu Val Asn Leu
225 230 235 240

Phe Glu Thr Trp Tyr Val Val Asp Ala Leu Trp Asn Glu Ser Lys Val
245 250 255

Leu Thr Thr Met Asp Ile Thr Thr Asp Gly Leu Gly Val Met Leu Leu
260 265 270

Phe Gly Asn Ala Val Trp Val Pro Phe Met Tyr Cys Leu Gln Ala Arg
275 280 285

Tyr Leu Ala Ser Phe Pro Val His Leu Gly Leu Leu Gly Ile Ala Gly
290 295 300

Val Leu Ala Val Gln Phe Thr Gly Tyr Ala Ile Phe Arg Gly Ala Asn
305 310 315 320

Asn Gln Lys Asn Ala Phe Arg Thr Asn Pro Ala Asp Pro Ala Val Ser
325 330 335

His Leu Lys Phe Met Thr Thr Lys Ser Gly Ser Lys Leu Leu Ile Ser
340 345 350

Gly Trp Trp Gly Val Ala Arg His Val Asn Tyr Phe Gly Asp Trp Ile
355 360 365

Met Ala Trp Ser Tyr Cys Leu Thr Thr Gly Phe Asn Thr Pro Leu Thr
370 375 380

Tyr Phe Tyr Val Ile Tyr Phe Gly Ile Leu Leu Leu His Arg Asp Arg
385 390 395 400

Arg Asp Glu Ala Lys Cys Arg Glu Lys Tyr Gly Lys Asp Trp Asp Arg
405 410 415

Tyr Cys Lys Val Val Lys Trp Arg Ile Ile Pro Gly Ile Tyr
420 425 430

<210> 10
<211> 365

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<212> PRT

<213> Arabidopsis thaliana

<400> 10

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Met Asp Leu Gly Val Leu Leu Pro Ser Leu Gln Ser Val Tyr Val Leu
 1      5      10      15
Val Phe Tyr Phe Val Tyr Leu Ala Val Ala Gly Glu Ile Leu Pro Gly
      20      25      30
Lys Val Ile Arg Gly Val Leu Leu Ser Asp Gly Ser Gln Leu Arg Tyr
      35      40      45
Arg Cys Asn Gly Leu Leu Ala Leu Ile Leu Leu Val Ala Ile Leu Gly
      50      55      60
Ile Cys Ala Lys Leu Gly Ile Val Ser Pro Leu Val Val Ala Asp Arg
      65      70      75      80
Gly Leu Glu Leu Leu Ser Ala Thr Phe Ile Phe Cys Val Leu Val Thr
      85      90      95
Leu Ala Leu Tyr Val Thr Gly Arg Ser Ser Ser Asn Lys Gly Ser Ser
      100      105      110
Leu Lys Pro His Val Ser Gly Asn Leu Val His Asp Trp Trp Phe Gly
      115      120      125
Ile Gln Leu Asn Pro Gln Phe Met Ser Ile Asp Leu Lys Phe Phe Phe
      130      135      140
Val Arg Ala Gly Met Met Gly Trp Leu Leu Ile Asn Leu Ser Ile Leu
      145      150      155      160
Ala Lys Ser Val Gln Asp Gly Ser Leu Ser Gln Ser Met Ile Leu Tyr
      165      170      175
Gln Ile Phe Cys Ala Leu Tyr Ile Leu Asp Tyr Phe Val His Glu Glu
      180      185      190
Tyr Met Thr Ser Thr Trp Asp Ile Ile Ala Glu Arg Leu Gly Phe Met
      195      200      205
Leu Val Phe Gly Asp Leu Leu Trp Ile Pro Phe Thr Phe Ser Ile Gln
      210      215      220
Gly Trp Trp Leu Leu His Asn Lys Val Glu Leu Thr Val Pro Ala Ile
      225      230      235      240
Val Val Asn Cys Leu Val Phe Leu Ile Gly Tyr Met Val Phe Arg Gly
      245      250      255
Ala Asn Lys Gln Lys His Ile Phe Lys Lys Asn Pro Lys Thr Pro Ile
      260      265      270
Trp Gly Lys Pro Pro Val Val Val Gly Gly Lys Leu Leu Val Ser Gly
      275      280      285
Tyr Trp Gly Ile Ala Arg His Cys Asn Tyr Leu Gly Asp Leu Met Leu
      290      295      300
Ala Leu Ser Phe Ser Leu Pro Cys Gly Ile Ser Ser Pro Val Pro Tyr
      305      310      315      320

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Phe Tyr Pro Ile Tyr Leu Leu Ile Leu Leu Ile Trp Arg Glu Arg Arg
325 330 335
Asp Glu Val Arg Cys Ala Glu Lys Tyr Lys Glu Ile Trp Ala Glu Tyr
340 345 350
Leu Arg Leu Val Pro Trp Arg Ile Leu Pro Tyr Val Tyr
355 360 365